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SEQUENCE ANALYSIS

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CLUSTAL W (1.82) Multiple Sequence Alignments

```
Sequence format is Pearson
Sequence 1: FixL          505 aa
Sequence 2: SEQ76        153 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 17
Guide tree          file created:  [/ebi/extserv/old-work/clust
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:                               Delayed
Sequence:2          Score:1222
Alignment Score 83
CLUSTAL-Alignment file created  [/ebi/extserv/old-work/clustal
```

clustalw-20030805-21191830.aln

CLUSTAL W (1.82) multiple sequence alignment

```
FixL          MAPTRVTHPPDDGRGEHFRVRIEGFGVGTWDLDLKTWALDWSDTAI
SEQ76          -----VLSEGEWQLVLHVWAKVEADVA-
                  .. * *: * *: * *: * *: *
FixL          LFLSRLEPDDRERVESAIKRVSERGGGFVSVFRVAGTSNAGQWIR/
```

```

SEQ76      -----

FixL      LSGIFLDIDEKQVEGALRTRETHLRSILHTIPDAMIVIDGHGII(
SEQ76      -----ILII
              :*:

FixL      LEAIGQNVNILMPEPDRSRHDSYISRYRTSDPHIIGIGRIVTGKI
SEQ76      FKHLKTEAEMKASEDLKKHGVTVLT-----ALGAILKKK-
              :: : :*: :*: :*: :*: :*: :*: :*: :*: :*: :*:

FixL      MQSGGEPYFTGFVRDLTEHQQTQARLQELQSELVHVSRLSAMGEM/
SEQ76      HEAELKPLAQ---SHATKHKIPIKYLEFISEAIIHVLHSRHPGDFC
              :: :* . *:* . * :.. :*: : *::

FixL      SNYMKGSRRLLAGSSDPNTPKVESALDRAAEQALRAGQIIRRLRDI
SEQ76      RKDIAAKYKELGYQG-----
              : : . : * . .

FixL      KLIEEAGALGLAGAREQNVQLRFSLDPGADLVLADRVQIQQLVNI
SEQ76      -----

FixL      ELVVTNTPAADDMIEVEVSDTGSGFQDDVIPNLFQTFFTTTKDTGMC
SEQ76      -----

FixL      GRMWAESNASGGATFRFTLPAADEN 505
SEQ76      -----



```

clustalw-20030805-21191830.dnd

(FixL:0.41176,SEQ76:0.41176);



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Search for

1: P23222. Sensor protein fixL...[gi:120207]

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LOCUS P23222 505 aa linear BCT 15-SEP-2003
 DEFINITION Sensor protein fixL.
 ACCESSION P23222
 VERSION P23222 GI:120207
 DBSOURCE swissprot: locus FIXL_BRAJA, accession P23222;
 class: standard.
 created: Nov 1, 1991.
 sequence updated: Nov 1, 1991.
 annotation updated: Sep 15, 2003.
 xrefs: gi: [39522](#), gi: [39523](#), gi: [3021308](#), gi: [3021311](#), gi: [27350985](#), gi: [27351017](#), gi: [7465577](#), pdb accession 1DRM, pdb accession 1LT0, pdb accession 1DP6, pdb accession 1DP8, pdb accession 1DP9, pdb accession 1LSV, pdb accession 1LSW, pdb accession 1LSX
 xrefs (non-sequence databases): InterProIPR003594, InterProIPR004358, InterProIPR003661, InterProIPR005467, InterProIPR001610, InterProIPR000700, InterProIPR000014, PfamPF02518, PfamPF00512, PfamPF00785, PfamPF00989, PRINTSPR00344, SMARTSM00387, SMARTSM00388, SMARTSM00086, SMARTSM00091, TIGRFAMsTIGR00229, PROSITEPS50109, PROSITEPS50113, PROSITEPS50112
 KEYWORDS Sensory transduction; Transferase; Kinase; Phosphorylation; Heme; Transmembrane; Inner membrane; Nitrogen fixation; Repeat; Iron transport; 3D-structure; Complete proteome.
 SOURCE Bradyrhizobium japonicum
 ORGANISM [Bradyrhizobium japonicum](#)
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.
 REFERENCE 1 (residues 1 to 505)
 AUTHORS Anthamatten,D. and Hennecke,H.
 TITLE The regulatory status of the fixL- and fixJ-like genes in Bradyrhizobium japonicum may be different from that in Rhizobium meliloti
 JOURNAL Mol. Gen. Genet. 225 (1), 38-48 (1991)
 MEDLINE [91155933](#)
 PUBMED [2000090](#)
 REMARK SEQUENCE FROM N.A.
 STRAIN=USDA 110spc4
 REFERENCE 2 (residues 1 to 505)
 AUTHORS Kaneko,T., Nakamura,Y., Sato,S., Minamisawa,K., Uchiyumi,T., Sasamoto,S., Watanabe,A., Idesawa,K., Iriguchi,M., Kawashima,K., Kohara,M., Matsumoto,M., Shimpo,S., Tsuruoka,H., Wada,T., Yamada,M. and Tabata,S.
 TITLE Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110
 JOURNAL DNA Res. 9 (6), 189-197 (2002)
 MEDLINE [22484998](#)
 PUBMED [12597275](#)

REMARK SEQUENCE FROM N.A.
STRAIN=USDA 110
REFERENCE 3 (residues 1 to 505)
AUTHORS Gong,W., Hao,B., Mansy,S.S., Gonzalez,G., Gilles-Gonzalez,M.A. and Chan,M.K.
TITLE Structure of a biological oxygen sensor: a new mechanism for heme-driven signal transduction
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (26), 15177-15182 (1998)
MEDLINE 99079986
PUBMED 9860942
REMARK X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 154-270.
REFERENCE 4 (residues 1 to 505)
AUTHORS Gong,W., Hao,B. and Chan,M.K.
TITLE New mechanistic insights from structural studies of the oxygen-sensing domain of Bradyrhizobium japonicum FixL
JOURNAL Biochemistry 39 (14), 3955-3962 (2000)
MEDLINE 20213243
PUBMED 10747783
REMARK X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 154-270.
COMMENT

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[FUNCTION] PUTATIVE OXYGEN SENSOR; MODULATES THE ACTIVITY OF FIXJ, A TRANSCRIPTIONAL ACTIVATOR OF NITROGEN FIXATION FIXK GENE. FIXL PROBABLY ACTS AS A KINASE THAT PHOSPHORYLATES FIXJ.
[ENZYME REGULATION] HEMOPROTEIN. THE HEME MOIETY REGULATES THE

KINASE ACTIVITY.

[SUBCELLULAR LOCATION] Integral membrane protein. Inner membrane.

[SIMILARITY] Contains 1 histidine kinase domain.

[SIMILARITY] Contains 2 PAS (PER-ARNT-SIM) dimerization domains.

[SIMILARITY] Contains 2 PAS-associated C-terminal (PAC) domains.

FEATURES	Location/Qualifiers
source	1..505 /organism="Bradyrhizobium japonicum" /db_xref="taxon:375"
gene	1..505 /gene="FIXL" /note="synonym: BLL2760"
Protein	1..505 /gene="FIXL" /product="Sensor protein fixL" /EC_number="2.7.3.-"
Region	14..85 /gene="FIXL" /region_name="Domain" /note="PAS 1."
Region	88..140 /gene="FIXL" /region_name="Domain" /note="PAC 1."
Region	141..208 /gene="FIXL" /region_name="Domain" /note="PAS 2."
Region	155..160 /gene="FIXL"

<u>Region</u>	/region_name="Beta-strand region" 161..162 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 164..168 /gene="FIXL"
<u>Region</u>	/region_name="Beta-strand region" 170..176 /gene="FIXL"
<u>Region</u>	/region_name="Helical region" 180..183 /gene="FIXL"
<u>Region</u>	/region_name="Helical region" 184..185 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 187 /gene="FIXL"
<u>Region</u>	/region_name="Beta-strand region" 188..191 /gene="FIXL"
<u>Region</u>	/region_name="Helical region" 194..195 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 196..210 /gene="FIXL"
<u>Site</u>	/region_name="Helical region" 200 /gene="FIXL"
<u>Region</u>	/site_type="metal-binding" /note="IRON (HEME AXIAL LIGAND)." 209..268 /gene="FIXL"
<u>Region</u>	/region_name="Domain" /note="PAC 2." 216..218 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 220..225 /gene="FIXL"
<u>Region</u>	/region_name="Beta-strand region" 227..228 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 231..243 /gene="FIXL"
<u>Region</u>	/region_name="Beta-strand region" 244..245 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 246..255 /gene="FIXL"
<u>Region</u>	/region_name="Beta-strand region" 257..268 /gene="FIXL"
<u>Region</u>	/region_name="Helical region" 269 /gene="FIXL"
	/region_name="Hydrogen bonded turn"

Region 288..503
/gene="FIXL"
/region_name="Domain"
/note="HISTIDINE KINASE."
Site 291
/gene="FIXL"
/site_type="phosphorylation"
/note="(AUTO-) (BY SIMILARITY)."

ORIGIN

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61 lflsrlepdd rervesaikr vsergggfdv sfrvagtsna gqwiraragl irdeagtarh
121 lsgifldide ekqvegalrt rethlrslh tipdamivid ghgiiqlfst aaerlfgwse
181 leaigqnvni lmpepdrsrh dsyisryrtt sdphiigigr ivtgkrrdgt tfpmhlsige
241 mqsggepyft gfvrldteh qtqarlqelq selvhvsrls amgemasala helnqplaa
301 snymkgsrrl lagssdpntp kvesaldras egalragqii rrlrldfvarg esekrvesls
361 klieeagalg lagareqnvq lrfsldpgad lvladrvtq qvlvnlfrna leamaqsqrr
421 elvvtntpaa ddmieevsd tsggfqddvi pnlftqftft kdtgmvgvls isrsiieahg
481 grmwaenas gqatfrftlp aaden
```

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Jul 30 2003 12:44:50